

| Result No | Score | Query Match | Length | PR | ID | Description |
|-----------|-------|-------------|--------|----|--------|--------------------|
| 1 | 55 | 100.0 | 586 | 4 | Q96C08 | Q96C08 homo sapien |
| 2 | 52 | 94.5 | 159 | 4 | Q9UJ26 | Q9UJ26 homo sapien |
| 3 | 52 | 94.5 | 586 | 11 | Q96T11 | Q96T11 mus muscula |
| 4 | 50 | 90.9 | 158 | 4 | Q9UJ27 | Q9UJ27 homo sapien |
| 5 | 48 | 87.3 | 455 | 11 | Q8VHP2 | Q8VHP2 rattus norv |
| 6 | 40 | 72.7 | 585 | 13 | Q96WF6 | Q96WF6 gallus gall |
| 7 | 39 | 70.9 | 429 | 4 | P78514 | P78514 homo sapien |
| 8 | 39 | 70.9 | 453 | 4 | Q9X854 | Q9X854 homo sapien |
| 9 | 39 | 70.9 | 634 | 9 | Q9XJ53 | Q9XJ53 bacterioph |
| 10 | 39 | 70.9 | 802 | 4 | Q9Y599 | Q9Y599 homo sapien |
| 11 | 38 | 69.1 | 130 | 16 | Q9K660 | Q9K660 bacillus ha |
| 12 | 38 | 69.1 | 150 | 16 | Q8UHE2 | Q8UHE2 agrobacteri |
| 13 | 37 | 67.3 | 111 | 9 | Q64106 | Q64106 bacterioph |
| 14 | 37 | 67.3 | 111 | 16 | Q34838 | Q34838 bacillus su |
| 15 | 37 | 67.3 | 217 | 17 | Q8U102 | Q8U102 pyrococcus |
| 16 | 37 | 67.3 | 231 | 17 | Q8U0V8 | Q8U0V8 pyrococcus |

97066 Q90026

92006Q90026

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A0 Q90J26;
DT 01 MAY-2000 (TEMBLrel. 13, Created)
DT 01 MAY-2000 (TEMBLrel. 13, Last sequence update)
DI 01 MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fadiel A., Chen Z.C., Nattoli F.,
RT "Mutation of ezrin gene in cancer."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189213; AAF03156.1; -.
DR InterPro: IPR000299; Hand.4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS00057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 19244 MW; 7C398388B7A70FA CRC64;

Query Match 94.5%; Score 52; DB 4; Length 159;
Best Local Similarity 90.9%; Pred. No. 0.034;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 1 ELMRLQDYEE 11
  |||||
DB 149 ELMRLQDYEE 159

RESULT 3
Q90J11
ID Q90J11 PRELIMINARY; PRI: 586 AA.
AC Q90J11;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DI 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone-0610037922, full insert sequence.
GN VIL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6J; TISSUE-KIDNEY;
RX MEDLINE 21085660; PubMed 11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hata A., Fujimishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Rono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kudoh P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,
RA Schirra L.M., Stanke J., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Haldarelli R., Harsh G.,
RA Blake J., Bellodi D., Benjuna N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Holtmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring R., Ringwald M., Rodriguez L., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilting L.,
RA Wyszynski R., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Bayazitaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK02766; BAB2341.1; -.
DR MGD: MGI:98941; VIL2.
DR InterPro: IPR000299; Band_4_1.

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DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_41; 1.
DR Pfam: PF00769; ERM; 1.
DR PRINTS: PR00935; HAND41.
DR SMART: SM00295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS00057; BAND_41_3; 1.
SQ SEQUENCE 586 AA; 69434 MW; 591A88F57F6DE3E CRC64;

Query Match 94.5%; Score 52; DB 11; Length 586;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 1 ELMRLQDYEE 11
  |||||
DB 346 ELMRLQDYEE 356

RESULT 4
Q90J27
ID Q90J27 PRELIMINARY; PRI: 158 AA.
AC Q90J27;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DI 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Z.C., Fadiel A., Nattoli F.;
RL "Ezrin gene mutation in ovarian cancer."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188897; AAF03155.1; -.
DR InterPro: IPR000299; Hand.4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS00057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 19089 MW; 86F92E1BC6F2957E CRC64;

Query Match 90.9%; Score 50; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 ELMRLQDYEE 10
  |||||
DB 149 ELMRLQDYEE 158

RESULT 5
Q8VHK3
ID Q8VHK3 PRELIMINARY; PRI: 455 AA.
AC Q8VHK3;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DI 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE Ezrin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRACUE-DAWLEY;
RA Gunn-Moore F.J., Tait S., Hroby P.J.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF450298; AAL47844.1; -.

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DP InterPro: IPR000294, Band 4.1
 DR InterPro: IPR000746; E2/rad/moesin.
 DR Pfam: PF00373; Band 4.1.
 DR Pfam: PF00769; ERM 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; R41; 1.
 DR PROSITE: PS00660; BAND_41_1, UNKNOWN_1.
 DR PROSITE: PS00661; BAND_41_2; UNKNOWN_1.
 DR PROSITE: PS00662; BAND_41_3; 1.
 FT NON_TER 455
 SQ SEQUENCE 455 AA; 54174 MW; 1FC9A95F4C7D5893 CRC64.

Query Match 87.3% Score 48, DB 13, Length 455,
 Best Local Similarity 81.8% Pred. No. 0.58;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
 ||| ||||| |||
 DB 346 ELMRLQDYEE 356

RESULT 6

Q9YGW6 PRELIMINARY: PRT; 585 AA.
 AC Q9YGW6
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ezrin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
 RX MEDLINE-99171943; PubMed-10051754;
 RA Takahashi M., Yamada M., Noda M.;
 RT "Specific expression of ezrin, a cytoskeletal membrane linker protein,
 R1 in a subset of chick retinotectal and sensory projections".
 RL Eur. J. Neurosci. 11:545-558(1999).
 DR EMBL: AB019790; BAA75497.1; 1.
 DR InterPro: IPR000299; Band 4.1.
 DR InterPro: IPR000749; E2/rad/moesin.
 DR Pfam: PF00373; Band 4.1; 1.
 DR Pfam: PF00769; ERM 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; R41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00662; BAND_41_3; 1.
 SQ SEQUENCE 585 AA; 69366 MW; 854C6348F7A3C4AC CRC64;

Query Match 72.7% Score 40; DB 13, Length 585,
 Best Local Similarity 70.0% Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 10
 ||| ||||| |||
 DB 346 ELLVRLQYEE 355

RESULT 7

P78514 PRELIMINARY: PRT; 429 AA.
 AC P78514; Q99844;
 DI 01-MAY-1997 (TrEMBLrel. 03, Created)
 DI 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DI 01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
 DE Hypothetical 48.1 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

NC Mammalia, Eutheria, Primates, Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Keen T.J.;
 KL Submitted (JUL 1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U85994; AAR61919.1; 1.
 DR EMBL: U85994; AAR61918.1; 1.
 DR EMBL: U85997; AAR46606.1; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 429 AA; 48892 MW; D6E3472A95971E9A CRC64;

Query Match 70.9% Score 39, DB 4, Length 429,
 Best Local Similarity 72.7% Pred. No. 29;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
 ||| ||||| |||
 DB 157 ELLVRLQYEE 167

RESULT 8

Q99854 PRELIMINARY: PRT; 453 AA.
 AC Q99854;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DI 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 51.1 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN;
 RA Keen T.J.;
 KL Submitted (JAN 1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87408; AAB47568.1; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 453 AA; 51050 MW; C5F53E164A83D418 CRC64;

Query Match 70.9% Score 39; DB 4; Length 453;
 Best Local Similarity 72.7% Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
 ||| ||||| |||
 DB 181 ELLVRLQYEE 191

RESULT 9

Q9AJS3 PRELIMINARY: PRT; 634 AA.
 AC Q9AJS3;
 DI 01-NOV-1999 (TrEMBLrel. 12, Created)
 DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative replication initiation protein p12.
 OS Bacteriophage PM2.
 OC Viruses; dsDNA viruses, no RNA stage; Corticoviridae; Corticovirus.
 OX NCBI_TaxID=10661;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kiwila H.M., Mannisto E.H., Kalkinen N., Bamford D.H.;
 RT "Purification and protein composition of PM2, the first lipid-
 RL containing bacterial virus to be isolated.";
 RL Virology 0:0-0(1999).
 RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE-99434236; PubMed-10502514;
RA Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Bamford J.K.;
R1 "The complete genome sequence of PM2, the first lipid containing
R2 bacterial virus to be isolated.";
R3 Virology 262:355-363(1999);
RN [1]
RP SEQUENCE FROM N.A.
RA Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Bamford J.K.H.;
R1 Submitted (MAY 1999) to the EMBL/GenBank/DBJ databases.
R2 EMBL: AF155037; AAD45543.1;
R3 SEQUENCE 634 AA; 72894 MW; 4F5CB0004FFH2506 CRC64;

Query Match 70.9%; Score 39; DB 9; Length 634;
Best local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 275 ELMVIRGQYEE 285

RESULT 10
QY699 PRELIMINARY: PPT: 802 AA
AC QY699;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE Transcriptional regulator, AsnC family.
GN PH responsive osteosarcoma H1 protein.
OS H1.
UN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OSTEOSARCOMA;
R1 MEDLINE-99246731; PubMed-10221542;
RA Adams A.E., Rosenblatt M., Suva L.J.;
R1 "Identification of a novel parathyroid hormone responsive gene in
R2 human osteoblastic cells.";
R3 Bone 24:305-313(1999).
R4 EMBL: AF095771; AAD25981.1;
R5 SEQUENCE 802 AA; 89844 MW; 3D7B534492C4CA92 CRC64;

Query Match 70.9%; Score 39; DB 4; Length 802;
Best local Similarity 72.7%; Pred. No. 54;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 540 ELMRLQDYEE 540

RESULT 11
QY660 PRELIMINARY: PPT: 140 AA
AC QY660;
DT 01-001-2000 (TEMBLrel. 15, Created)
DT 01-001-2000 (TEMBLrel. 15, Last sequence update)
DE Hypothetical protein B03872.
GN B03872.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group, Bacillales;
OC Bacillaceae; Bacillus.
CX NCBI_TaxID=8665;
RN [1]
RP SEQUENCE FROM N.A.
R1 STRAIN-C-125 / JCM 9154;
R2 MEDLINE-20512582; PubMed-11058132;
RA Takami H., Nakasone K., Takaki Y., Macho G., Sasaki K., Masui N.,

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RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horiuchi K.;
R1 "Complete genome sequence of the alkaliphilic bacterium Bacillus
R2 halodurans and genomic sequence comparison with Bacillus subtilis.";
R3 Nucleic Acids Res. 28:4317-4331(2000).
R4 EMBL: AP001520; HA07591.1;
R5 InterPro: IPR004360; Gly_bico_diox.
R6 Pfam: PF00903; Glyoxalase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 130 AA; 15271 MW; B39FE8EED72DF09F CRC64;

Query Match 69.1%; Score 38; DB 16; Length 130;
Best local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LRLODYEE 11
DB 78 LRVDYEE 85

RESULT 12
QY802 PRELIMINARY: PPT: 150 AA
AC QY802;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Transcriptional regulator, AsnC family.
GN AT00740 OR AGR_C1339.
OS Agrobacterium tumefaciens (strain C58 / ATCC 34970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
CX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608550; PubMed-11743193;
RA Wood D.W., Setubal J.C., Kaul P., Monks D.F., Kitajima J.P.,
RA Okora V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D., Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayian I., Levy K., Li M.-J., McLelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., You H., Tao Y., Hiddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm R., Liag I., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tinney S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
R1 "The genome of the natural genetic engineer Agrobacterium tumefaciens
R2 C58.";
R3 Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608551; PubMed-11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo H., Goldman H.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Roumelio K., Gordon J., Vaudin M., Jarchock O., Pipp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz H.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cleo C., Slater S.;
R1 "Genome sequence of the plant pathogen and biotechnology agent
R2 Agrobacterium tumefaciens C58.";
R3 Science 294:2323-2328(2001).
R4 EMBL: AF009042; AAL41756.1;
R5 EMBL: AE008008; AAK86548.1;
R6 Complete proteome.
SQ SEQUENCE 150 AA; 16748 MW; 4BE5AR39E46125FD CRC64;

Query Match 69.1%; Score 38; DB 16; Length 150;
Best local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMLPLQDYEE 11
DB 106 LMLRLDMEK 115

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RESULT 13
064106 PRELIMINARY: PPT: 111 AA
AC 064106
DT 01-AUG-1998 (TREMblrel. 07, Created)
DI 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Hypothetical 12.5 kDa protein.
GN YOPW.
OS Bacteriophage SPB02.
OC VIRUSES; dsDNA viruses, no RNA stage, Caudovirales; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauei C.,
RA Karamata D.
RT "the complete nucleotide sequence of the Bacillus subtilis SPB02
RT prophage."
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases
DR EMBL: AF029913; ANL3966.1;
KW Hypothetical protein.
SQ SEQUENCE 111 AA; 12549 MW; F1886HRC44AF778 CRC64;

Query Match 67.3%; Score 37; DB 9; Length 111;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 20 EKLKISDYEE 30
IIII:IIII

RESULT 14
034838 PRELIMINARY: PPT: 111 AA.
AC 034838
DT 01-JAN-1998 (TREMblrel. 05, Created)
DI 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DI 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE YOPW protein.
GN YOPW.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/volastriidum group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunz F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Becker M.G., Bessieres P., Bolotin A., Borchert S.,
RA Horst R., Housier L., Brans A., Braun M., Brignell S.C., Brown S.,
RA Brouillet S., Brusch C.V., Caldwell R., Capuano V., Carter N.M.,
RA Choi S.K., Cudini J., Cummings I.F., Cummings N.J., Daniel P.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.E.,
RA Eulian K.D., Errington J., Fabre C., Ferraric E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Grandi N.,
RA Kim S.Y., Glaser P., Goffeau A., Gollightly E.J., Groll G.,
RA Gutseppe G., Guy R.J., Hagi K., Halcch J., Harwood G.R., Heide A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koehler P., Kunitzstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neuge B., O'Keilly M., Ogilwara A., Oudega H., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presser E., Rajic P., Rameil B., Rappoport S., Roy M., Rylands S.,
RA Rieger M., Pivolar C., Roche E., Roche P., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter P., Scofield F.,
RA Sekiguchi J., Skowska A., Soror S.J., Serror P., Shin H.S., Soldo B.,

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RA Sorokin A., Taroni E., Takagi T., Takahashi H., Takemura K.,
RA Takeuchi M., Yamakoshi A., Tanaka T., Terstra P., Iomoni A.,
RA Tetsu V., Uchiyama S., Vandenbol M., Vardier F., Vassarotti A.,
RA Viari A., Wambull R., Wedler E., Wedler H., Weizenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yamamoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RN [2]
RP Nature 390:249-256(1997).
RP SEQUENCE FROM N.A.
RP STRAIN=168;
RA Kunz F., Ogasawara N., Yoshikawa H., Zanchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z99114; CAB13966.1;
DR EMBL: Z99115; CAB13992.1;
KW Complete proteome.
SQ SEQUENCE 111 AA; 12549 MW; F1886HRC44AF778 CRC64;

Query Match 67.3%; Score 37; DB 16; Length 111;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 20 EKLKISDYEE 30
IIII:IIII

RESULT 15
080102 PRELIMINARY: PPT: 217 AA.
AC 080102
DI 01-JUN-2002 (TREMblrel. 21, Created)
DI 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DI 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical protein PF1113.
GN PF1113.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VCL / DSM 1638 / ATCC 43587 / JCM 8422;
RA Weiss P.R., Dunn P.M., Poth F.I., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF010221; AAL81237.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 217 AA; 24508 MW; 91F253BF57C38451 CRC64.

Query Match 67.3%; Score 37; DB 17; Length 217;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 169 EIVPFLDYEE 179
IIII:IIII

Search completed, January 16, 2003, 16:55:45
Job time : 41.0714 secs

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